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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=29; hr=17; min=14; sec=58; ms=546; ]

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\*\*\*\*\*

Reviewer Comments:

<110> ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY  
MELNICK, Ari M.  
LICHT, Jonathan D.  
PRIVÉ, Gilbert G.  
AHMAD, Khaja Farid

Please remove the foreign accent mark from the fourth applicant's name:  
foreign accent marks are non-ASCII characters, and cannot be processed.

<210> 10  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> consensus sequence

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> amino acid residue is Leu, Gly, or Tyr

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> amino acid residue is Val, Ile, or Arg

<220>  
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<222> (3)..(3)  
<223> amino acid residue is Ala, Thr, or Ser

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<222> (4)..(4)  
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<223> amino acid residue is Ala, Met, or Thr

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<220>  
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<223> amino acid residue is Arg or Gly

<400> 10

Leu	Val	Ala	Thr	Val	Lys	Glu	Ala	Gly	Arg	Ser	Ile	His	Glu	Ile	Pro
1				5					10					15	

Arg

The above <220>-<223> sections stating that the amino acids at those locations can also represent another amino acid are incorrect (e.g., for location 1, amino acid residue is Leu, Gly, or Tyr). "Leu" at location 1 can only represent itself. Please use "Xaa's" instead, and explain which amino acid residues they can represent.

\*\*\*\*\*

Validated By CRFValidator v 1.0.3

Application No: 10582662 Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010  
Finished: 2008-05-28 14:21:47.829  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms  
Total Warnings: 20  
Total Errors: 0  
No. of SeqIDs Defined: 34  
Actual SeqID Count: 34

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010  
Finished: 2008-05-28 14:21:47.829  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms  
Total Warnings: 20  
Total Errors: 0  
No. of SeqIDs Defined: 34  
Actual SeqID Count: 34

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<210> 1  
<211> 17  
<212> PRT  
<213> Homo sapiens

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Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro  
1 5 10 15

Arg

<210> 2  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 2

Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro  
1 5 10 15

Arg

<210> 3  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 3

Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro  
1 5 10 15

Gly

<210> 4  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 4

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile  
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Pro Arg Glu Glu Leu

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<210> 5  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 5

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Gln Asp Ile  
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<210> 6  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 6

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val  
1 5 10 15

Pro Gly Pro Ser Pro  
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<210> 7  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 7

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu Pro Leu  
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<210> 8  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 8

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile  
1 5 10 15

Pro Arg Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr  
20 25

<210> 9  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 9

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val  
1 5 10 15

Pro Gly Pro Ser Pro Asn Glu Glu Asn Asn Gly Lys  
20 25

<210> 10  
<211> 17  
<212> PRT  
<213> Artificial

<220>  
<223> consensus sequence

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> amino acid residue is Leu, Gly, or Tyr

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> amino acid residue is Val, Ile, or Arg

<220>  
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<222> (3)..(3)  
<223> amino acid residue is Ala, Thr, or Ser

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> amino acid residue is Thr or Glu

<220>  
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<222> (5)..(5)  
<223> amino acid residue is Val or Ile

<220>  
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<222> (6)..(6)  
 <223> amino acid residue is Lys or Ile  
  
 <220>  
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 <222> (7)..(7)  
 <223> amino acid residue is Glu or Ser  
  
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 <223> amino acid residue is Ala, Met, or Thr

<220>  
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 <222> (9)..(9)  
 <223> amino acid residue is Gly or Ala

<220>  
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 <223> amino acid residue is Arg or Pro

<220>  
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 <222> (12)..(12)  
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<220>  
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 <223> amino acid residue is His or Trp

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<220>  
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<400> 10

Leu	Val	Ala	Thr	Val	Lys	Glu	Ala	Gly	Arg	Ser	Ile	His	Glu	Ile	Pro
1				5					10					15	

Arg

<210> 11  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 11

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Ser  
1 5 10 15

Asp Val Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr  
20 25 30

Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr  
35 40 45

Val Leu Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln  
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro  
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn  
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu  
100 105 110

Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser  
115 120 125

Glu

<210> 12  
<211> 127  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic mutant

<400> 12

Gly Ser Ala Asp Ser Gln Ile Gln Phe Thr Arg His Ala Ser Asp Val  
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Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val  
 20 25 30

Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu  
 35 40 45

Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys  
 50 55 60

Arg Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly  
 65 70 75 80

Phe Asn Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg  
 85 90 95

Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met  
 100 105 110

Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser Glu  
 115 120 125

<210> 13  
 <211> 93  
 <212> DNA  
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<220>  
 <223> oligonucleotide for plasmid construction

<400> 13  
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 agctgcggca cacgcccagag ctgcccctgg ccc 93

<210> 14  
 <211> 93  
 <212> DNA  
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<220>  
 <223> oligonucleotide for plasmid construction

<400> 14  
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 gagcggcccg cctccttcac cgtggccacc agc 93

<210> 15  
<211> 93  
<212> DNA  
<213> Artificial

<220>

<223> oligonucleotide for plasmid construction

<400> 15  
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agctgcggca cagccccgag ctgcccctgg ccc 93

<210> 16  
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<212> DNA  
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<220>

<223> oligonucleotide for plasmid construction

<400> 16  
tcgagggcca ggggcagctc gggcgtgtgc cgcagctcct cagctgcagc tgcattggatg 60  
  
gagcggcccg cctccttcac cgtggccacc agc 93

<210> 17  
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<212> DNA  
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<220>

<223> primer

<400> 17  
catcctgggc cattacctta 20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial

<220>

<223> primer

<400> 18  
tctctctctg catcttgggg 20

<210> 19  
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<220>

<223> primer

<400> 19

gactctgaag agccacctgc

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<210> 20

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<223> primer

<400> 20

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<210> 21

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<223> primer

<400> 21

ccggacctaa tccctcactc

20

<210> 22

<211> 20

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 22

cacaccgatg cagctttcta

20

<210> 23

<211> 21

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 23

aaaggaaccc cacgaagtgt t

21

<210> 24

<211> 22

<212> DNA  
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<220>  
<223> primer

<400> 24  
tcaagggcat atcctacaac aa

22

<210> 25  
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<220>  
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<400> 25  
acgatgctgg gtcaggtatc

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<220>  
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<400> 26  
agtgactagg gcgctgtgtt

20

<210> 27  
<211> 22  
<212> DNA  
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<220>  
<223> primer

<400> 27  
gggttcttag aagtggatgc gc

22

<210> 28  
<211> 20  
<212> DNA  
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<220>  
<223> primer

<400> 28  
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<210> 29  
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<212> DNA  
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<220>  
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<400> 29  
cgatgaggag ttctgggatg t

21

<210> 30  
<211> 21  
<212> DNA  
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<220>  
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<400> 30  
tttctggggg ctctgtggac t

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<210> 31  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 31

Cys Ala Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp  
1 5 10 15

Val Val Pro Gly Pro Ser Pro Asn Glu  
20 25

<210> 32  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 32

Arg Ser Glu Ile Ile Ser Thr Ala Pro Ala Ser Ala Val Ala Pro Gly  
1 5 10 15

Pro

<210> 33  
<211> 17

<212> PRT  
<213> Homo sapiens

<400> 33

Arg Ser Glu Ile Ile Ser Thr Ala Pro Trp Ser Ser Val Val Pro Gly  
1                   5                   10                   15

Pro

<210> 34  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 34

Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro Gly  
1                   5                   10                   15

Pro